

GenCore version 6.3
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OM protein - protein search, using SW model

Run on: June 15, 2009, 01:03:29 ; Search time 73 Seconds
(without alignments)
1137.335 Million cell updates/sec

Title: US-10-561-671-2
Perfect score: 531
Sequence: 1 TSNVIFTVNNAATTVYQQNVY.....RTYTVPFSSSTGSYTANWNVP 99

Scoring table: BL0SUM62

Searched: 4548778 seqs, 838641292 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 95%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200812::*
1:: geneseq::*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	DB			
1	531	100.0	99	1	ADW21532		Bacillus
2	531	100.0	99	1	ADW25806		Bacillus
3	531	100.0	99	1	AEA06468		Aea06468
4	531	100.0	99	1	AEB72819		Carbohydr
5	531	100.0	99	1	AEI54700		Glucoamy1
6	531	100.0	99	1	AOG56868		Aog56868
7	531	100.0	613	1	ADW21550		Bacillus
8	531	100.0	613	1	ADW71773		Anoxybaci

ALIGNMENTS

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ALWZ133Z

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ΤΖΑΤΖΙ

(commonly known as glucan 1,4-alpha-glucosidase, EC 3.2.1.3). The invention discloses amino acid sequences for functional CBM (SEQ ID Nos 1 -3), enzymes having alpha-amylase activity (SEQ ID Nos 4-18), and enzymes having alpha-amylase activity with a functional CBM (SEQ ID Nos 19-22). Also described are: (i) a process (M2) for the production of high fructose starch-based syrup (HFSS), where a soluble starch hydrolysate produced by method (M1) is subjected to conversion into HFSS, such as high fructose corn syrup (HFCS), (ii) a process (M3) for production of a fermentation product, where a soluble starch hydrolysate produced by method (M1) is subjected to fermentation into a fermentation product, such as citric acid, monosodium glutamate, gluconic acid, sodium gluconate, calcium gluconate, potassium gluconate, glucono delta lactone, sodium erythorbate, itaconic acid, lactic acid, gluconic acid, ketones, amino acids, glutamic acid (sodium monoglutamate), penicillin, tetracycline, enzymes, vitamins, such as riboflavin, B12, beta-carotene or hormones, (iii) a process (M4) for production of fuel or potable ethanol, where a soluble starch hydrolysate produced by method (M1) is subjected to fermentation into ethanol, (iv) use of an enzyme having alpha-amylase activity in a process for hydrolysis of starch, and (v) use of an enzyme having alpha-amylase activity in a process for hydrolysis of granular starch. Method (M1) is useful for producing a soluble starch hydrolysate which is useful for production of high fructose starch-based syrup (HFSS), a fermentation product, fuel or potable ethanol. An enzyme having alpha-amylase is useful for the hydrolysis of granular starch. The hydrolysates are useful as sweeteners or as precursors for other saccharides, such as fructose. This sequence represents a carbohydrate-binding module (CBM).

XX SQ Sequence 99 AA;

Query Match 100.0%; Score 531; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.6e-50;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

29-JUL-2003; 2003US-0490751P.
14-OCT-2003; 2003US-0511044P.
24-OCT-2003; 2003DK-00001568.
27-OCT-2003; 2003US-0514854P.
10-MAY-2004; 2004US-0569862P.

PA (NOVO) NOVOZYMES AS.
PA (NOVO) NOVOZYMES NORTH AMERICA INC.

Taira R, Tkagi S, Hjort C, Vikso-Nielsen A, Allain E, Udagawa H;

WPI; 2005-101485/11.

New hybrid enzyme comprising a catalytic module with alpha-amylase activity and a carbohydrate-binding module, useful for liquefying starch for subsequent fermentation to produce e.g., ethanol, citric acid, vitamins, or antibiotics.

Claim 1; SEQ ID NO 10; 102pp; English.

CC such as riboflavin, B12, beta-carotene or hormones. The starch slurry is
CC contacted with a polypeptide comprising a carbohydrate-binding module,
CC but not catalytic module. The hybrid enzyme or variant enzyme is useful
CC for preparing a dough-based product, which involves adding the enzyme to
CC the dough. This sequence represents a CBM.
XX

SQ Sequence 99 AA;

Query	1 TSNVTFTVNNNATTVYQQNYYVVGNIPELGNWNIANAIQMTPSSYPTWKT	TVSLPQGKAIE	60
Best Local Similarity	100.0%	Score 531; DB 1; Length 99;	
Matches	99; Conservative 0; Mi smatches 0;	Pred. No. 1.6e-50; Indels 0; Gaps 0;	
Db	1 TSNVTFTVNNNATTVYQQNYYVVGNIPELGNWNIANAIQMTPSSYPTWKT	TVSLPQGKAIE	60
QY	61 FKFIIKKDSAGNVIWENIANRTYTVPFSSSTGSYTA	NWNVP 99	
Db	61 FKFIIKKDSAGNVIWENIANRTYTVPFSSSTGSYTA	NWNVP 99	

RESULT 3

AEA06468

ID AEA06468 standard; protein; 99 AA.

XX

AC AEA06468;

XX

DT 28-JUL-2005 (First entry)

XX

DE Bacillus, carbohydrate binding module.

XX

KW glucoamylase; carbohydrate binding module; fermentation.

XX

XX

OS Bacillus sp.
XX WO2005045018-A1.
PN 19-MAY-2005.
XX PF 27-OCT-2004; 2004WO-US035991.
XX PR 28-OCT-2003; 2003US-0515017P.
XX PA (NOVO) NOVOZYMES NORTH AMERICA INC.
PA (NOVO) NOVOZYMES AS.
XX PI Borchert T, Danielsen S, Allain E;
XX DR WPI; 2005-347063/35.
XX PT New hybrid enzyme comprising an amino acid sequence of a catalytic module
PT having glucoamylase activity and a sequence of a carbohydrate-binding
module, useful for producing a fermentation product such as ethanol, or
PT syrup.
XX Disclosure; SEQ ID NO 4; 105pp; English.
XX PT The invention relates to a hybrid enzyme which comprises an amino acid
PT sequence of a catalytic module having glucoamylase activity and an amino
PT acid sequence of a carbohydrate-binding module. The hybrid enzyme is
PT useful for producing a fermentation product such as ethanol, or syrup.
PT The present sequence represents the amino acid sequence of a *Bacillus*
PT glucoamylase, carbohydrate binding module.
XX SQ Sequence 99 AA;

XX	PR	16-JAN-2004;	2004US-0537071P.
XX	PR	14-DEC-2004;	2004US-0636013P.
XX	PA	(NOVO) NOVOZYMES	NORTH AMERICA INC.
XX	PA	(NOVO) NOVOZYMES	AS.
XX	PI	Allain E, Wenger KS,	Bisgaard-Frantzen H;
XX	DR	WPI;	2005-542205/55.
XX	DR	N-PSDB;	AEB72816.
XX	PCT	Producing fermentation product e.g. ethanol from starch-containing material involves saccharifying the material with specific glucoamylase, at temperature below initial gelatinization temperature of the material and fermenting.	
XX	PS	Disclosure; SEQ ID NO 15;	96pp; English.
XX	CC	This sequence represents a carbohydrate-binding module (CBM) from carbohydrate-binding module Family 20. This sequence may be used in the construction of a hybrid alpha-amylase protein which may be used in the method of the invention. The method for producing a fermentation product from milled starch-containing material involves: saccharifying milled starch-containing material with the glucoamylase from the fungi <i>Athelia rolfsii</i> , at temperature below the initial gelatinization temperature of starch containing material; and fermenting using a fermenting medium. The process is carried out for 1 - 250, especially 80 - 130 hours, at pH of 3 - 7, especially 4 - 5. The dry solid (DS) content in the process is 20 - 55 (preferably 25 - 40, especially 30 - 35) wt.%. The sugar concentration is kept below 3 wt.% during saccharification and fermentation. A slurry of water and milled starch-containing material is prepared before step (a). The milled-starch-containing material is prepared by milling starch-	

CC containing material to a particle size of 0.1 - 0.5 mm. The
 CC saccharification is carried out simultaneously. The fermentation is
 CC carried out at 28 - 36, especially 32 deg C. The glucoamylase is present
 CC in an amount of 0.01 - 10, especially 0.1 - 0.5 AGU/g DS. The
 CC fermentation product is recovered after fermentation. The process is
 CC carried out in the presence of a protease (preferably acid protease,
 CC especially fungal acid protease). The starch-containing material is
 CC obtained from tubers, roots, stems, seeds or whole grains of corn, cobs,
 CC wheat, barley, rye, milo, sago, cassava, manioc, tapioca, sorghum, rice
 CC or potatoes (preferably cereals). The method of the invention is for
 CC producing a fermentation product e.g. alcohol such as ethanol selected
 CC from fuel ethanol, potable ethanol and industrial ethanol. The method
 CC produces fermentation product without gelatinization of the starch-
 CC containing material; and produces ethanol in higher yield
 XX

SQ Sequence 99 AA;

Query	1 TSNVTFTVNNATTVYQQNYYVVGNIPELGNWNIANAIQMTPTSSYPTWKT	Length	99;
Best	100.0%;	Score	531;
Local	100.0%;	DB	1;
Similarity	Pred. No. 1.6e-50;		
Matches	99;	Mismatches	0;
	Conservative	Indels	0;
		Gaps	0;
Db	1 TSNVTFTVNNATTVYQQNYYVVGNIPELGNWNIANAIQMTPTSSYPTWKT		60
Qy	61 FKFIIKKDSAGNVIWENIANRTYTVPFSSTGSYTA		99
Db	61 FKFIIKKDSAGNVIWENIANRTYTVPFSSTGSYTA		99

RESULT 5
 AEI54700
 ID AEI54700 standard; protein; 99 AA.
 v.v

XXX AEI54700;
XXX DT 24-AUG-2006 (first entry)
XXX DE Glucoamylase carbohydrate-binding domain SEQ ID NO:6.
XXX KW textile; glucoamylase.
XXX OS Bacillus sp.
XXX PN WO2006065579-A2.
XXX PD 22-JUN-2006.
XXX PF 01-DEC-2005; 2005WO-US044044.
XXX PR 02-DEC-2004; 2004US-0632611P.
XXX PA (NOVO) NOVOZYMES NORTH AMERICA INC.
XXX PI Wu G, Liu J, Salmon S;
XXX DR WPI; 2006-454552/46.
XXX PCT Desizing of sized fabric that contains starch or star
XXX PCT the manufacture of fabric, involves incubation of the
XXX PCT aqueous acidic treating solution containing alpha-amy
XXX PCT Disclosure; SEQ ID NO 6; 114pp; English.
XXX PCT The invention relates to desizing of a sized fabric th
XXX PCT or starch derivatives during manufacture, by incubati
XXX PCT on a aqueous acidic solution containing alpha-amy
XXX PCT Disclosure; SEQ ID NO 6; 114pp; English.

CC in an aqueous treating solution with a pH of 1-5 (preferably 2-4) and
CC comprising an alpha-amylase. The alpha-amylase (preferably acid alpha-
CC amylase) is of bacterial or fungal, such as filamentous fungus, origin.
CC The alpha-amylase is a derived from **Aspergillus**, **Rhizomucor**, or
CC **Meripilus**. The bacterial alpha-amylase is derived from a strain of
CC **Bacillus** and is preferably AA560 alpha-amylase. The alpha-amylase is a
CC hybrid enzyme having a carbohydrate-binding domain (CBD) (preferably
CC starch-binding domain of fungal or bacterial origin derived from strains
CC of **Aspergillus**, **Athelia**, or **Talaromyces**). The alpha-amylase having a CBD
CC comprises a linker between the alpha-amylase and CBD or starch-binding
CC domain, where the linker is derived from strain of **Athelia** or
CC **Aspergillus**. Alternatively, the alpha-amylase is a hybrid alpha-amylase
CC comprising a catalytic domain (CD) from **Rhizomucor pusillus** alpha-amylase
CC that has a carbohydrate-binding domain (CBD) from the glucoamylase of
CC **Athelia rolfsii**. The method is useful for desizing of sized fabrics (e.g.
CC fabric made from fibres of natural, man-made or animal origin such as
CC cotton fabric, denim, linen, ramie, viscose, lyocell, cellulose acetate,
CC silk, or wool; or polyester fibers of man-made or natural origin such as
CC poly(ethylene terephthalate) or poly(lactic acid); or fibers of nylon,
CC acrylic, or polyurethane; polyester containing fabric or garment that
CC consists of 100% polyester; or the polyester fabric consisting of
CC polyester blend, such as polyester and cellulose blend, including
CC polyester and cotton blends; polyester and wool blend; polyester and silk
CC blend; polyester and acrylic blend; polyester and nylon blend; polyester,
CC nylon and polyurethane blend; polyester and polyurethane blend, rayon
CC (viscose), cellulose acetate and tencel) during manufacture of fabric.
CC The process facilitates desizing of the fabric during manufacture of new
CC fabrics with traditional sizing/desizing equipments, hence no additional
CC process equipment is required. In the process, demineralization takes
CC place simultaneously and/or after desizing of the sized fabric in the
CC same treating solution as compared to the prior art, thus the process
CC saves time, and reduces cost of e.g. acids and manpower for acid addition
CC as the pH adjustment step is eliminated. This sequence is a glucoamylase
CC ~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~

CC carbohydrate-binding domain.

XXX

Sequence 99 AA:

Query Match	100.0%	Score	531;	DB	1;	Length	99;
Best Local Similarity	100.0%	Pred.	No.	1.6e-50;			
Matches	99;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

QY	1 TSNVIFTVNNAATTVYGVNVYVVGNIPELGNWNIANAIIQMTIPSSSYPTWKTIVSLPQGKAE	60
Db	1 TSNVIFTVNNAATTVYGVNVYVVGNIPELGNWNIANAIIQMTIPSSSYPTWKTIVSLPQGKAE	60

QY 61 EKFIKKDSAGNVIWENIANRTTYTVPFSSSTGSYTA
NNVP 99
Db 61 EKFIKKDSAGNVIWENIANRTTYTVPFSSSTGSYTA
NNVP 99

DECTET

AOG56868

ID A0G56868 Standard; protein; 99 AA.

XXX

AC AOG56868;

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01-1981-2000 (1981-2000) (1981-2000) (1981-2000)

AA DE Bacillus sp. alpha-amylase CBD domain protein.
 XX XX
 KW Alpha-amylase; endo-alpha-amylase; 1, 4-alpha-D-glucan-glucano-hydrolase;
 KW enzyme; EC 3.2.1.1.

Bacillus sp. OS

WO2007149699-A2.

XX PD 27-DEC-2007.
XX PF 06-JUN-2007; 2007WO-US070485.
XX PR 21-JUN-2006; 2006US-0815788P.
XX PA (NOVO) NOVOZYMES NORTH AMERICA INC.
PA (NOVO) NOVOZYMES AS.
XX PI Liu J, Salmon S, Wu G;
XX DR WPI; 2008-D53563/25.
XX PT Combined desizing and scouring of a sized fabric containing starch or
PT starch derivatives during manufacture of a fabric by incubating the sized
PT fabric in an aqueous treating solution comprising an acid amylase and
PT acid scouring enzyme.
XX PS Disclosure; SEQ ID NO 6; 43pp; English.
XX CC The present invention provides a process for combined desizing and
CC scouring of a sized fabric containing starch or starch derivatives during
CC manufacture of a fabric. The process involves incubating said sized
CC fabric in an aqueous treating solution having a pH in the range between 1
CC and 7, which aqueous treating solution comprises an alpha-amylase such as
CC acid alpha-amylase (endo-alpha-amylase, 1, 4-alpha-D-glucan-glucano-
CC hydrolase) or hybrid alpha-amylase containing a carbohydrate-binding
CC domain (CBD) and at least one other acid enzyme (such as cellulase,
CC pectinase, lipase, xylanase and protease) facilitating said other fabric
CC treatment steps. Acid amylases of the invention are of bacterial or
CC fungal origin such as filamentous fungus origin. The present sequence is
CC a *Bacillus* sp. alpha-amylase (EC 3.2.1.1) CBD domain protein.
vv

XX	SQ	Sequence 99 AA;						
		Query Match	100.0%;	Score 531;	DB 1;	Length 99;		
		Best Local Similarity	100.0%;	Pred. No. 1.6e-50;				
		Matches 99;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
	QY	1 TSNVTFVNNAATTVYQQNYYVVGNIPELGNWNIANAIQMTPSSYPTWKTIVSLPQGKAI	60					
	Db	1 TSNVTFVNNAATTVYQQNYYVVGNIPELGNWNIANAIQMTPSSYPTWKTIVSLPQGKAI	60					
	QY	61 FKFIIKKDSAGNVIWENIANRTYTVPFSSSTGSYTA	99					
	Db	61 FKFIIKKDSAGNVIWENIANRTYTVPFSSSTGSYTA	99					
		RESULT 7						
		ADW21550						
		ID ADW21550	standard;	protein;	613 AA.			
		XX						
		AC ADW21550;						
		XX						
		DT 24-MAR-2005	(first entry)					
		XX						
		DE Bacillus alpha-amylase for granular starch hydrolysis.						
		XX						
		KW Starch;	sugar;	high fructose starch-based syrup;				
		KW high fructose corn syrup;	fermentation;	fuel;	ethanol;	hydrolysis;		
		KW sweetener;	alpha-amylase;	enzyme;	EC 3.2.1.1;			
		KW carbohydrate-binding module.						
		XX						
		OS Bacillus.						
		OS Synthetic.						
		vv						

XX WO2004113551-A1.

XX PN

XX PD 29-DEC-2004.

XX PF 25-JUN-2004; 2004WO-DK000456.

XX PR 25-JUN-2003; 2003DK-00000949.

XX PR 24-OCT-2003; 2003DK-00001568.

XX PA (NOVO) NOVOZYMES AS.

XX PI Viksoe-Nielsen A, Andersen C, Pedersen S, Hjort C;

XX DR 2005-075255/08.

XX PT Producing soluble starch hydrolysate comprises subjecting aqueous granular starch slurry below initial gelatinization temperature of granular starch to action of Glycoside Hydrolase Family13 enzyme, and fungal amylase.

XX PS Claim 4; SEQ ID NO 20; 68pp; English.

XX CC The invention relates to a method (M1) of producing a soluble starch hydrolysate. The method involves subjecting an aqueous granular starch slurry to the action of a first and second enzyme, where the first enzyme is member of the Glycoside Hydrolase Family13, having alpha-1,4-glucosidic hydrolysis activity and comprising a functional carbohydatabinding module (CBM), and a second enzyme chosen from a fungal alpha-amylase (EC 3.2.1.1), a beta-amylase (EC 3.2.1.2) or glucoamylase (commonly known as glucan 1,4-alpha-glucosidase, EC 3.2.1.3). The invention discloses amino acid sequences for functional CBM (SEQ ID Nos 1-3), enzymes having alpha-amylase activity (SEQ ID Nos 4-18), and enzymes having alpha-amylase activity (SEQ ID Nos 19-22).

having alpha-amylase activity with a functional CBM (SEQ ID Nos 19-22). Also described are: (i) a process (M2) for the production of high fructose starch-based syrup (HFSS), where a soluble starch hydrolysate produced by method (M1) is subjected to conversion into HFSS, such as high fructose corn syrup (HFCS), (ii) a process (M3) for production of fermentation product, where a soluble starch hydrolysate produced by method (M1) is subjected to fermentation into a fermentation product, such as citric acid, monosodium glutamate, gluconic acid, sodium gluconate, calcium gluconate, potassium gluconate, glucono delta lactone, sodium erythorbate, itaconic acid, lactic acid, gluconic acid, ketones, amino acids, glutamic acid (sodium monoglutamate), penicillin, tetracycline, enzymes, vitamins, such as riboflavin, B12, beta-carotene or hormones, (iii) a process (M4) for production of fuel or potable ethanol, where a soluble starch hydrolysate produced by method (M1) is subjected to fermentation into ethanol, (iv) use of an enzyme having alpha-amylase activity in a process for hydrolysis of starch, and (v) use of an enzyme having alpha-amylase activity in a process for hydrolysis of granular starch. Method (M1) is useful for producing a soluble starch hydrolysate which is useful for production of high fructose starch-based syrup (HFSS), a fermentation product, fuel or potable ethanol. An enzyme having alpha-amylase is useful for the hydrolysis of granular starch. The hydrolysates are useful as sweeteners or as precursors for other saccharides, such as fructose. This sequence represents an alpha-amylase with a functional CBM.

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Query Match          100.0%;  Score 531;  DB 1;  Length 613;
Best Local Similarity 100.0%;  Pred. No. 1.7e-49;
Matches 99;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

515 TSNVIFTVNNTATTIVYGONVYVGNIPELGNWNIANAIOMTPSSYPTWKTITVSLPOGKAIIE 574
DB

QY	61	FKFIKKDSAGNVIWENIANRTTYTVPFSSSTGSYTA NWNVP	99
	575	FKFIKKDSAGNVIWENIANRTTYTVPFSSSTGSYTA NWNVP	613
Db			

FFT	Domain	/note= "region specifically claimed in claim 16"
FFT	485. .613	/note = carbohydrate binding domain
FFT	Region	485. .583
FFT	XX	/note= "region specifically claimed in claim 25"
PN	WO20050001064-A2.	
XXX	06-JAN-2005.	
PD		
XXX		
PF	25-JUN-2004;	2004WO-US023031.
XX		
PR	25-JUN-2003;	2003DK-00000949.
PR	25-JUN-2003;	2003US-0482589P.
PR	24-OCT-2003;	2003DK-00001568.
PR	27-OCT-2003;	2003US-0514854P.
PR	12-NOV-2003;	2003US-0519554P.
XX		
PA	(NOVO) NOVOZYME AS.	
PA	(NOVO) NOVOZYME NORTH AMERICA INC.	
XX		
PI	Hoff T, Andersen C,	Spedler T, Pedersen S, Vikso-Nielsen A;
PI	Schaffer T, Liu J;	
XX		
DR	WPI; 2005-075552/08.	
DR	N-PSDB; ADW71772.	
XX		
PPT	Novel polypeptide having alpha-amylase activity and/or carbohydra-	
PPT	binding affinity, useful in preparing detergent composition and com-	
PPT	and in textile desizing.	
XX		
PS	Claim 1; SEQ ID NO 6; 79pp; English.	
XX		

CC This invention describes a novel polypeptide isolated from *Anoxybacillus*
CC *flavithermus* (*Bacillus flavithermus*) which has alpha-amylase activity
CC and/or carbohydrate-binding affinity. The novel polypeptide is useful 1)
CC in cleaning or detergent composition, preferably laundry or dish wash
CC compositions optionally with a surfactant), 2) for desizing and treating
CC textiles, fabrics, yarn or garments, 3) for preparing a dough-based
CC product with improved elasticity, firmness, softness and moistness, 4)
CC for liquefaction of starch, 5) in ethanol and fuel production from starch
CC or whole grains 6) in beer making or brewing 7) pulp and paper production
CC or 8) sweetener production. This sequence represents a novel
CC *Anoxybacillus flavithermus* alpha-amylase.
XX

SQ Sequence 613 AA;

Query	Match	100.0%;	Score	531;	DB	1;	Length	613;	
Best	Local	Similarity	100.0%;	Pred.	No.	1.7e-49;			
Matches	99;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	TSNVTFTVNNATTVYQQNYYVVGNIPELGNWNIANAIQMTPSSYPTWKT							60
		TVSLPQGKAIE							
Db	515	TSNVTFTVNNATTVYQQNYYVVGNIPELGNWNIANAIQMTPSSYPTWKT							574
		TVSLPQGKAIE							
QY	61	FKFIKKDSAGNVIWENIANRTYTVPFSSSTGSYTA							99
		NWNVP							
Db	575	FKFIKKDSAGNVIWENIANRTYTVPFSSSTGSYTA							613
		NWNVP							

Search completed: June 15, 2009, 01:04:43
Job time : 74 secs